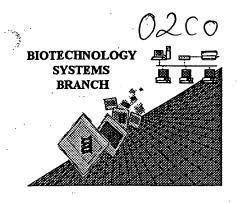
RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/968,44

Art Unit / Team No.: 0 / 1/12

Date Processed by STIC: //13/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

	ERROR DETECTED	SUGGESTED	CORRECTION	SERIAL NUMBER: U_{I}^{o}	1468,147
ATTN:	NEW RULES CASES: P	LEASE DISREGA	ARD ENGLISH "AL	PHA" HEADERS, WHICH WERE INSERTED	BY PTO SOFTWARE
	Wrapped Nucleics	The number/text	at the end of each	line "wrapped" down to the next line.	
٠	mapped made	This may occur i	f your file was retrie	ved in a word processor after creating it.	
		Please adjust yo	our right margin to	3, as this will prevent "wrapping".	
	Managed Aminos	The amine acid (number/lext at the s	nd of each line "wrapped" down to the next lin	ne.
2	Wrapped Aminos	This man seems	if your file was retrie	eved in a word processor after creating it.	
		Please adjust yo	our right margin to .	3, as this will prevent "wrapping".	
3	Incorrect Line Length	The rules require	that a line not exc	eed 72 characters in length. This includes spa	ices.
				o acid is misaligned. This may be caused by t	
4	Misaligned Amino Acid Numbering	between the nun	nbering. It is recomn	nended to delete any tabs and use spacing be	tween the numbers.
e	Non-ASCII	This file was not	saved in ASCII (DC	S) text, as required by the Sequence Rules.	
3 <u> </u>	Non-Asch	Please ensure ye	our subsequent sub	mission is saved in ASCII text so that it can be	e processed.
6	Variable Length	Sequence(s)	contain n's or Xa	a's which represented more than one residue.	
· —		As per the rules.	each n or Xaa can	only represent a single residue.	
		Please present t	he maximum numbe	er of each residue having variable length and	
		indicate in the (i	x) feature section th	at some may be missing.	
7	Patentin ver. 2.0 "bug"	A "bug" in Patent	In version 2.0 has	caused the <220>-<223> section to be missing	from amino acid
	•	sequence(s)	. Norma	ally. Patentin would automatically generate this	s section from the
		previously code	d nucleic acid seque	ence. Please manually copy the relevant <220)>-<223> section
			nt amino acid sequ		
8	Skipped Sequences	Sequence(s)	_ missing. If intenti	onal, please use the following format for each	skipped sequence:
	(OLD RULES)	(2) INFORMATIO	ON FOR SEQ ID NO	D:X:	
	,	(i) SEQUENCE (CHARACTERISTIC	S:(Do not Insert any headings under "SEQUEI	NCE CHARACTERISTICS")
	•	(xi) SEQUENCE	DESCRIPTION:SE	Q ID NO:X:	
			s intentionally ski		
•		Please also adju	st the "(iii) NUMBEF	R OF SEQUENCES:" response to include the	skipped sequence(s).
9	Skipped Sequences	Sequence(s)	_ missing. If intenti-	onal, please use the following format for each	skipped sequence.
	(NEW RULES)	<210> sequenc			
1	,	<400> sequenc			
Ì		000			
10 (Use of n's or Xaa's	Use of n's and/or	· Xaa's have been d	etected in the Sequence Listing.	
· · ·	(NEW RULES)	Use of <220> to	<223> Is MANDATO	ORY if n's or Xaa's are present.	
	(NEW NOCEO)	In <220> to <223	> section, please e	xplain location of n or Xaa, and which residue	n or Xaa represents.
11	Use of <213>Organism	Sequence(s)	are missing th	nis mandatory field or its response.	
	(NEW RULES)				•
12	Use of <220>Feature	Sequence(s)	_ are missing the <	220>Feature and associated headings.	
	(NEW RULES)	Use of <220> to	<223> is MANDATO	ORY if <213>ORGANISM is "Artificial" or "Unk	nown ⁻
	•	Please explain s	ource of genetic r	naterial in <220> to <223> section.	
		(See "Federal	Register, 6/01	/98, Vol. 63, No. 104, pp. 29631-32)	(Sec. 1.823 of new Rules)
13	Patentin ver. 2.0 "bug"	Please do not us	se "Copy to Disk"	function of Patentin version 2.0. This cause	es a corrupted
	559	file, resulting in m	nissing mandatory n	umeric identifiers and responses (as indicated	l on raw sequence listing).
		Instead, please u	se "File Manager" o	or any other means to copy file to floppy disk.	
		A	<s-biotechnology s<="" td=""><td>ystems Branch- 5/15/99</td><td></td></s-biotechnology>	ystems Branch- 5/15/99	

OIPE

PAGE:

RAW SEQUENCE LISTING

PATENT APPLICATION US/09/468,147

DATE: 01/13/2000

TIME: 14:21:59

Input Set: I468147.RAW

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

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                                                               Corrected Diskette Needed
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41	Gln	Thr	Glu	Ile	Leu	Ile	Asn	Leu	Met	Gln	Pro	Arg	Gln	Leu	Val-	Phe	
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53	Cys	Phe	Leu	Arg	Pro	Val	Gly	Arg		Val	Gln	Arg	${\tt Trp}$		Ser	Ala	
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60		130					135					140					
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62		Phe	Ala	Ala	GIu		GIA	vaı	Ата	ьeu	_	ser	Leu	HIS	Asp		
63	145		4			150			_ 4		155					160	500
64			-	gat	_	_		_	_	_	-					_	528
65	Trp	Pro	Ala	Asp		Ата	GIU	Ата	Met		Arg	HIS	GIY	хаа		Arg	
66	++~		~~~	~~~	165	a aa	att	999	aat	170	at a	ata	ata	a aa	175	~~~	576
67	-		_	gca Ala	_												576
68 69	пеп	TYL	AIA	180	шеu	птэ	пец	FIO	185	GIU	vai	пеа	пец	190	FIO	GIY	
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71				Thr		_			_			_		_	_	_	021
72	1111	- 7 -	195		****	501	- / -	200					205				
73	at.t.	αta		tac	gag	aac	gat		agt.	aca	aac	tat		cat	gat	atc	672
74	_	_		Tyr			-		_						-	_	
75		210					215				•	220			_		
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77				Arg													
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89	Ser	Pro	Ser	Leu	Phe	Pro	Ser	Ala	Cys	Ser	Thr	Lys	Ser	Thr	Phe	His	

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95	Leu	Asp	Asp	Gln		Phe	Cys	Cys	Ser	Arg	Leu	Met	Thr	Tyr		Arg	
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189				820					825					830			

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191	Ala Phe	-	o Thr	Glu	Phe	Ile	Met	Arg	Glu	Gly		Ala	Ala	\mathtt{Tyr}	
192		835				840					845				
193	_	g acc co						_	_						2592
194		ı Thr P	o Arg	Pro		Ile	His	Ala	Val		Pro	Asp	Tyr	Arg	
195	850				855					860	•				
196	gtt gag	_	_	_				_							2640
197	Val Glu	ı Gln A	n Pro	_	Arg	Leu	Glu	Ala		Tyr	Arg	Glu	Thr		
198	865			870					875					880	
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207		915				920					925				2020
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209	Ala Asr	_	O ALA	GII		vaı	ьeu	Thr	тте		GIU	Asp	THE	Ald	
210	930				935					940			~ ~	~~~	2000
211	cgt acg	_	_	-	_			_	_	-					2880
212	Arg Thi	Ala A	in Leu		ьеu	GIU	TTE	Asp	955	Ala	1111	GIU	vai	960	
213	945	. +~+ ~,		950	200	2 t a	200	aat		a++	~+ <i>~</i>	a aa	+ > +		2928
214	cgt gct Arg Ala			_			-							_	2920
215 216	Arg Are	Cys A.	.a Giy 965	Сув	1111	TIE	PET	970	СТУ	116	vai	HID	975	GIII	
217	ttt acc			000	~~~	+ 00	~~~		+ 42	200	+ a a	ata		cac	2976
218	Phe Thi			_		_		_							2370
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486

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Leu Arg Arg Arg

Leu Arg Arg Arg

Leu Arg 487 488

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                   Ala Ile Ser Ile Ser Phe Trp Pro Gln Thr Thr Thr Pro Thr Ser
       512
                                                               220
       513
                                           215
                   Val Asp Met Asn Ser Ile Thr Ser Thr Asp Val Arg Ile Leu Val Gln
       514
                                                           235
       515
                                       230
                   Pro Gly Ile Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr
       516
       517
                                       245
                                                           250
                   Arg Asn Gln Gly Trp Arg Ser Val Glu Thr Thr Gly Val Ala Glu Glu
       518
       519
                                                           265
                   Glu Ala Thr Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Pro Val
       520
                                      275
                                                          280
       521
                   Asn Ser Tyr Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly Leu Leu Asp
       522
       523
                                           295
                   Phe Ala Leu Glu Leu Glu Phe Arg Asn Leu Thr Pro Gly Asn Thr Asn
       524
       525
                   Thr Arg Val Ser Arg Tyr Thr Ser Thr Ala Arg His Arg Leu Arg Arg
       526
      527
                                       325
                  Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Ala Ala Thr Arg Phe
       528
                                       340
                                                           345
      529
                  Met Lys Asp Leu His Phe Thr Gly Thr Asn Gly Val Gly Glu Val Gly
       530
                                                          360
      531
                                      355
                  Arg Gly Ile Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly
      532
                                                               380
      533
                                           375
                  Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr
      534
                                       390
                                                           395
      535
                  Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr
      536
                                                           410
                                       405
       537
                  Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Thr Ile Pro His
      538
```

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PATENT APPLICATION US/09/468,147

Input Set: I468147.RAW

	539	415				_	420					425	_				
	540	_	Ile	Asp	Leu			Ser	Arg	Val			Gln	Asp	Tyr		
	541	30					435					140					445
	542	Gln	His	Glu	Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro
	543		450					455					460				
	544	Phe	Ser	Val	Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala
	545	465			1		470					475					
W>	546 ND 1	Ala	Glu	Tyr	(Xaa)	Gln	Thr	Thr	Tyr	Gly	Ser	Ser	Thr	Asn	Pro	Met	Tyr
	547	480					485					490					
	547	Val	Ser	Asp	Thr	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly	Ala	Gln	Ala
	549	495					500					505					
	550 (1/2)	Val	Ala	Arg	Ser	Leu	Asp	Trp	Ser	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro
	551 C 10 10 10 10 10 10 10 10 10 10 10 10 10	10				5	515					520					525
	552 M	Leu	Thr	Thr	Ile	Gln	${\tt Gln}$	Tyr	Ser	Lys	Lys	Phe	Tyr	Val	Leu	Pro	Leu
	553 WM of		530					535					540				
W>	554	Xaa	Gly	Lys	Leu	Ser	Phe	Trp	Glu	Ala	Gly	Thr	Thr	Lys	Ala	Gly	Tyr
	555 /	545	'				550					555					
	556	Pro	Tyr	Asn	Tyr	Asn	Thr	Thr	Ala	Ser	Asp	Gln	Ile	Leu	Ile	Glu	Asn
	557	560					565					570					
	558	Ala	Ala	Gly	His	Arg	Val	Ala	Ile	Ser	Thr	Tyr	Thr	Thr	Ser	Leu	Gly
	559	575					5,80	'/				585					
W>	560	Ala	Gly	Pro	Thr	Ser	Kaa	\$er	Ala	Val	Gly	Val	Leu	Ala	Pro	His	Ser
	561	90				5	595~	/			(500				6	505
	562	Ala	Leu	Ala	Val	Leu	Glu	Asp	Thr	Val	Asp	Tyr	Pro	Ala	Arg	Ala	His
	563		610					615					620				
	564	Thr	Phe	Asp	Asp	Phe	Cys	Pro	Glu	Cys	Arg	Thr	Leu	Gly	Leu	${\tt Gln}$	Gly
	565	625					630					635					
	566	Cys	Ala	Phe	Gln	Ser	Thr	Ile	Ala	Glu	Leu	Gln	Arg	Leu	Lys	Met	Lys
	567	640					645					650					
	568	Val	Gly	Lys	Thr	Arg	Glu	Ser									
	569	655	_	-		_	660										

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

PAGE:

VERIFICATION SUMMARY PATENT APPLICATION US/09/468,147 DATE: 01/13/2000 TIME: 14:21:59

Line	?	Error/Warning	Original Text	
479	E	Number of Bases conflict w/ Running Total	. 2360	
495	E	Invalid/Missing Amino Acid Numbering	65 70	
497	E	Invalid/Missing Amino Acid Numbering	80 85 9	
499	E	Invalid/Missing Amino Acid Numbering	95 100 10	
		"N" or "Xaa" used: Feature required	Ala Glu Tyr Xaa Gln Thr Thr Tyr Gly Ser S	
554	W	"N" or "Xaa" used: Feature required	Xaa Gly Lys Leu Ser Phe Trp Glu Ala Gly T	
560	W	"N" or "Xaa" used: Feature required	Ala Gly Pro Thr Ser Xaa Ser Ala Val Gly V	